The understanding of emerging collective behaviors in biomolecular complexes represent a major challenge in modern biophysics. As a first step toward the study of such processes we have applied multi-resolution nonlinear dimensionality reduction to obtain reliable low-dimensional representations and models for the dynamics of apparently high-dimensional complex systems such as proteins in a biological environment. Although still preliminary, the results clearly show that the proposed methods can efficiently find low dimensional representations of a complex process such as protein folding. (Received September 23, 2009)